



PCT09

## RAW SEQUENCE LISTING

DATE: 05/07/2002

PATENT APPLICATION: US/09/913,878A

TIME: 14:47:11

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3 <110> APPLICANT: Universit. degli Studi di Roma La Sapienza  
4 Macino Giuseppe  
5 Cogoni Carlo  
7 <120> TITLE OF INVENTION: Isolation and characterization of a N. crassa silencing  
8 gene and uses thereof  
10 <130> FILE REFERENCE: macino2  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/913,878A  
C--> 13 <141> CURRENT FILING DATE: 2002-03-22  
15 <150> PRIOR APPLICATION NUMBER: RM99A000117  
16 <151> PRIOR FILING DATE: 1999-02-22  
18 <160> NUMBER OF SEQ ID NOS: 2  
20 <170> SOFTWARE: PatentIn Ver. 2.1  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 8045  
24 <212> TYPE: DNA  
25 <213> ORGANISM: Neurospora crassa  
27 <220> FEATURE:  
28 <221> NAME/KEY: CDS  
29 <222> LOCATION: (2447)..(6655)  
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36 ccgaataggt tcgtacgctg tccccctttag ggggctggtt taacaggag acagggtaca 180  
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40 ctgaggggtcc atacaacat acatgctgtg tagagagtgg tgggaatatt agaggttact 300  
42 ttgagagttt ctgaagagat tgagactgta ggtacgttca tttatcgggtg cgacgagaat 360  
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46 atgtgtcggc ctgagactgt ccaatggacc aatggtaagg cgtgagcggc gaggggggtc 480  
48 aacttgaggt taatgtacac agtacttgag gctgtagcgg gcagcgggaag catccgtcct 540  
50 cgaatggaca ttcccaagcc agccaacact ggtgtccatt taaaagcgtt ttctccatgg 600  
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110 atctcacagt cgcttgtcc tccttttcgg tgggtgctgc ttttatcatg ccttatcgct 2400
112 aaccgggttg tatactctac tccaggcccc atctcccacg gcacaa atg aac cct 2455
113                                     Met Asn Pro
114                                     1
116 att act cct agg aag agg aat agc ccc gtc gag gaa atc ata aac cgg 2503
117 Ile Thr Pro Arg Lys Arg Asn Ser Pro Val Glu Glu Ile Ile Asn Arg
118      5                      10                      15
120 ctc aat aac gac tac aac ctg ggc ctc cag tgt gtc gca gac aca act 2551
121 Leu Asn Asn Asp Tyr Asn Leu Gly Leu Gln Cys Val Ala Asp Thr Thr
122 20                      25                      30                      35
124 ctc acc ccc cac cgc cgg aag gag ctg gcc gag agt gac gag gat ttc 2599
125 Leu Thr Pro His Arg Lys Glu Leu Ala Glu Ser Asp Glu Asp Phe
126      40                      45                      50
128 ggt cgc cat gac aag atc tac aga gcc ctg aac ttt ctc tac tgg cgg 2647
129 Gly Arg His Asp Lys Ile Tyr Arg Ala Leu Asn Phe Leu Tyr Trp Arg
130      55                      60                      65
132 aag gat gac tcc ctg aac cag gca gaa gcc aac ttc ttc atc gag gcc 2695
133 Lys Asp Asp Ser Leu Asn Gln Ala Glu Ala Asn Phe Phe Ile Glu Ala
134      70                      75                      80
136 aaa gct gcg agc tcg aac tgg gtg ccc aaa gcc cac gcc gac cct gac 2743
137 Lys Ala Ala Ser Ser Asn Trp Val Pro Lys Ala His Ala Asp Pro Asp
138      85                      90                      95
140 acg ctt ccg tgg tcc aag gaa cct ccc cgc gcc gct act gcc ggc caa 2791
141 Thr Leu Pro Trp Ser Lys Glu Pro Pro Arg Ala Ala Thr Ala Gly Gln
142 100                      105                      110                      115
144 caa tgg gca ttg cag act gtg ttg ctc gag gtg ctt aat agg ttt atg 2839
145 Gln Trp Ala Leu Gln Thr Val Leu Leu Glu Val Leu Asn Arg Phe Met
146      120                      125                      130
148 cca cct ccc aat aac aca cca ggt cga acg ttt ggc aga act cta agc 2887
149 Pro Pro Pro Asn Asn Thr Pro Gly Arg Thr Phe Gly Arg Thr Leu Ser
150      135                      140                      145
152 ggc cca agt ggc ctg agc cgc cca acc tct acc aac acc aaa cgc aag 2935
153 Gly Pro Ser Gly Leu Ser Arg Pro Thr Ser Thr Asn Thr Lys Arg Lys
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156	gat gag ccc gcc aat gtc act ttc gct gat ccg ccc aaa cgc tcg ttg	2983		
157	Asp Glu Pro Ala Asn Val Thr Phe Ala Asp Pro Pro Lys Arg Ser Leu			
158	165	170	175	
160	act cgc tct gcc aca ggt cct cct att cac ggc gcg gcg ata ccc cta	3031		
161	Thr Arg Ser Ala Thr Gly Pro Pro Ile His Gly Ala Ala Ile Pro Leu			
162	180	185	190	195
164	aag ttc ccc gat cca gtg aat acc ggt tcc aaa cga cca tct ctc gag	3079		
165	Lys Phe Pro Asp Pro Val Asn Thr Gly Ser Lys Arg Pro Ser Leu Glu			
166	200	205	210	
168	agt gag aat ctc aat cag tgc acc aag cgg gcc aag ggc aag ctg tct	3127		
169	Ser Glu Asn Leu Asn Gln Cys Thr Lys Arg Ala Lys Gly Lys Leu Ser			
170	215	220	225	
172	gat aat gtt gcc gct gcc gcc gcc ccg ccc gtg cct att gcg agc gct	3175		
173	Asp Asn Val Ala Ala Ala Ala Ala Pro Pro Val Pro Ile Ala Ser Ala			
174	230	235	240	
176	ttg gac aag gta ccg act cga agg cat gcc aat acg aga gat ccc acg	3223		
177	Leu Asp Lys Val Pro Thr Arg Arg His Ala Asn Thr Arg Asp Pro Thr			
178	245	250	255	
180	gcg aca ggt cat aga cga gcg gac cag gtg gat tcc ttt gat aca tct	3271		
181	Ala Thr Gly His Arg Arg Ala Asp Gln Val Asp Ser Phe Asp Thr Ser			
182	260	265	270	275
184	caa ggc act tcc tat ggt tcg agt gtc ttc agc gct tgc cgt cac aat	3319		
185	Gln Gly Thr Ser Tyr Gly Ser Ser Val Phe Ser Ala Cys Arg His Asn			
186	280	285	290	
188	cag agc act acc cag agt agt ttt gag gct cct cct tca cag ccc aga	3367		
189	Gln Ser Thr Thr Gln Ser Ser Phe Glu Ala Pro Pro Ser Gln Pro Arg			
190	295	300	305	
192	gag aag cgg cct gtg gat gcc acg gtc ttt gag gct gga cac ttg att	3415		
193	Glu Lys Arg Pro Val Asp Ala Thr Val Phe Glu Ala Gly His Leu Ile			
194	310	315	320	
196	gag tct cct agc aaa gga aga aca acc aag tcc cac ata gat aac cag	3463		
197	Glu Ser Pro Ser Lys Gly Arg Thr Thr Lys Ser His Ile Asp Asn Gln			
198	325	330	335	
200	ccc ctt tca tcg tct tcc cag ggt gaa act tcg ttc agc act tac tat	3511		
201	Pro Leu Ser Ser Ser Ser Gln Gly Glu Thr Ser Phe Ser Thr Tyr Tyr			
202	340	345	350	355
204	gag tcg ttt cca agt tcc ggc ggc gag ggc gca att ccc gag ccg agt	3559		
205	Glu Ser Phe Pro Ser Ser Gly Gly Glu Gly Ala Ile Pro Glu Pro Ser			
206	360	365	370	
208	cgc tca aat gga ctg gct cgg agc gaa gaa agc gct cga tct cag gtt	3607		
209	Arg Ser Asn Gly Leu Ala Arg Ser Glu Glu Ser Ala Arg Ser Gln Val			
210	375	380	385	
212	caa gtt cat gcc ccg gtg gtt gca gct cgg ctg aga aat att tgg ccg	3655		
213	Gln Val His Ala Pro Val Val Ala Ala Arg Leu Arg Asn Ile Trp Pro			
214	390	395	400	
216	aaa ttt ccc aaa tgg cta cac gaa gct cct ctc gct gtt gca tgg gaa	3703		
217	Lys Phe Pro Lys Trp Leu His Glu Ala Pro Leu Ala Val Ala Trp Glu			
218	405	410	415	

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222	420					425					430					435	
224	ctg	ggc	cta	aag	tac	gac	cct	tcc	tgg	tct	acc	gcg	cgc	gat	gtc	aca	3799
225	Leu	Gly	Leu	Lys	Tyr	Asp	Pro	Ser	Trp	Ser	Thr	Ala	Arg	Asp	Val	Thr	
226					440						445					450	
228	gat	atc	tgg	aag	act	ctc	tac	cgg	ctt	gat	gct	ttc	cgt	ggt	aaa	ccc	3847
229	Asp	Ile	Trp	Lys	Thr	Leu	Tyr	Arg	Leu	Asp	Ala	Phe	Arg	Gly	Lys	Pro	
230					455					460					465		
232	ttt	cca	gaa	aag	ccg	ccc	aac	gac	gtg	ttc	gtg	acc	gca	atg	acg	ggc	3895
233	Phe	Pro	Glu	Lys	Pro	Pro	Asn	Asp	Val	Phe	Val	Thr	Ala	Met	Thr	Gly	
234			470						475						480		
236	aac	ttt	gag	agc	aaa	ggt	agt	gcc	gtt	gtt	ctc	tct	gct	gtt	cta	gac	3943
237	Asn	Phe	Glu	Ser	Lys	Gly	Ser	Ala	Val	Val	Leu	Ser	Ala	Val	Leu	Asp	
238			485					490							495		
240	tac	aat	ccg	gac	aac	tcg	cct	act	gcg	ccc	ctt	tac	ctt	gtg	aag	ctg	3991
241	Tyr	Asn	Pro	Asp	Asn	Ser	Pro	Thr	Ala	Pro	Leu	Tyr	Leu	Val	Lys	Leu	
242	500					505					510					515	
244	aag	ccg	ctc	atg	ttc	gag	cag	ggc	tgt	cga	ctc	acc	cgt	cgg	ttc	ggt	4039
245	Lys	Pro	Leu	Met	Phe	Glu	Gln	Gly	Cys	Arg	Leu	Thr	Arg	Arg	Phe	Gly	
246					520					525						530	
248	cct	gat	agg	ttt	ttc	gag	atc	ctt	ata	ccg	tcg	cct	acg	agc	acc	agc	4087
249	Pro	Asp	Arg	Phe	Phe	Glu	Ile	Leu	Ile	Pro	Ser	Pro	Thr	Ser	Thr	Ser	
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252	cca	agt	gta	ccg	ccg	gtg	gtc	agc	aaa	caa	cca	ggt	gcg	gtc	gaa	gaa	4135
253	Pro	Ser	Val	Pro	Pro	Val	Val	Ser	Lys	Gln	Pro	Gly	Ala	Val	Glu	Glu	
254			550					555							560		
256	gtc	atc	cag	tgg	ctc	acg	atg	ggg	caa	cat	tct	ctt	gta	ggc	cgc	caa	4183
257	Val	Ile	Gln	Trp	Leu	Thr	Met	Gly	Gln	His	Ser	Leu	Val	Gly	Arg	Gln	
258			565					570							575		
260	tgg	cgc	gct	ttc	ttc	gcc	aaa	gat	gcc	gga	tac	agg	aaa	cct	ctc	agg	4231
261	Trp	Arg	Ala	Phe	Phe	Ala	Lys	Asp	Ala	Gly	Tyr	Arg	Lys	Pro	Leu	Arg	
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264	gag	ttc	cag	ctc	cgc	gcc	gag	gac	ccg	aaa	ccc	atc	atc	aag	gag	aga	4279
265	Glu	Phe	Gln	Leu	Arg	Ala	Glu	Asp	Pro	Lys	Pro	Ile	Ile	Lys	Glu	Arg	
266					600					605						610	
268	gtc	cac	ttc	ttt	gcc	gag	acc	ggc	att	acg	ttc	cga	cct	gat	gtg	ttc	4327
269	Val	His	Phe	Phe	Ala	Glu	Thr	Gly	Ile	Thr	Phe	Arg	Pro	Asp	Val	Phe	
270					615					620						625	
272	aag	acg	aga	tct	gtc	gtt	ccg	gca	gag	gaa	cct	gta	gag	caa	cgg	acc	4375
273	Lys	Thr	Arg	Ser	Val	Val	Pro	Ala	Glu	Glu	Pro	Val	Glu	Gln	Arg	Thr	
274			630					635							640		
276	gag	ttc	aaa	gtt	agt	caa	atg	ctg	gac	tgg	ctc	ctg	caa	ctc	gac	aac	4423
277	Glu	Phe	Lys	Val	Ser	Gln	Met	Leu	Asp	Trp	Leu	Leu	Gln	Leu	Asp	Asn	
278			645					650							655		
280	aac	act	tgg	cag	ccg	cac	ctc	aag	ttg	ttc	tcc	cgt	atc	cag	ctc	ggt	4471
281	Asn	Thr	Trp	Gln	Pro	His	Leu	Lys	Leu	Phe	Ser	Arg	Ile	Gln	Leu	Gly	
282	660					665					670					675	
284	ctg	agt	aag	aca	tat	gcc	att	atg	aca	ttg	gag	cct	cac	cag	atc	aga	4519

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289	His	His	Lys	Thr	Asp	Leu	Leu	Ser	Pro	Ser	Gly	Thr	Gly	Glu	Val	Met	
290				695					700					705			
292	aat	gac	ggt	gta	ggc	cgc	atg	tcg	cga	agc	gtg	gcc	aag	agg	ata	cgc	4615
293	Asn	Asp	Gly	Val	Gly	Arg	Met	Ser	Arg	Ser	Val	Ala	Lys	Arg	Ile	Arg	
294			710					715					720				
296	gat	gtt	ctc	ggt	ttg	ggt	gat	gtg	ccc	tct	gct	gtg	caa	ggg	cgg	ttt	4663
297	Asp	Val	Leu	Gly	Leu	Gly	Asp	Val	Pro	Ser	Ala	Val	Gln	Gly	Arg	Phe	
298		725					730					735					
300	ggt	tcg	gcc	aag	gga	atg	tgg	gtt	atc	gac	gtt	gac	gac	aca	ggc	gat	4711
301	Gly	Ser	Ala	Lys	Gly	Met	Trp	Val	Ile	Asp	Val	Asp	Asp	Thr	Gly	Asp	
302	740				745						750				755		
304	gag	gat	tgg	atc	gag	aca	tac	ccg	tcc	cag	cgc	aag	tgg	gaa	tgc	gac	4759
305	Glu	Asp	Trp	Ile	Glu	Thr	Tyr	Pro	Ser	Gln	Arg	Lys	Trp	Glu	Cys	Asp	
306				760						765				770			
308	ttc	gtt	gat	aaa	cat	caa	cgt	acc	ctc	gaa	gtc	cgg	agc	gtg	gct	tct	4807
309	Phe	Val	Asp	Lys	His	Gln	Arg	Thr	Leu	Glu	Val	Arg	Ser	Val	Ala	Ser	
310			775					780						785			
312	gaa	ctg	aag	tca	gct	ggt	ctc	aac	cta	cag	ctg	tta	cct	gtc	ctg	gaa	4855
313	Glu	Leu	Lys	Ser	Ala	Gly	Leu	Asn	Leu	Gln	Leu	Leu	Pro	Val	Leu	Glu	
314			790					795					800				
316	gat	aga	gcc	agg	gac	aag	gtg	aag	atg	cgc	cag	gca	atc	ggt	gac	cgt	4903
317	Asp	Arg	Ala	Arg	Asp	Lys	Val	Lys	Met	Arg	Gln	Ala	Ile	Gly	Asp	Arg	
318		805					810					815					
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321	Leu	Ile	Asn	Asp	Leu	Gln	Arg	Gln	Phe	Ser	Glu	Gln	Lys	His	Ala	Leu	
322	820				825					830				835			
324	aat	cgc	cca	gtg	gaa	ttt	cgc	caa	tgg	gtt	tac	gag	agt	tat	tcc	agt	4999
325	Asn	Arg	Pro	Val	Glu	Phe	Arg	Gln	Trp	Val	Tyr	Glu	Ser	Tyr	Ser	Ser	
326				840					845					850			
328	cgc	gca	act	cga	gtc	agc	cac	ggc	cgt	gtg	cct	ttt	ctt	gct	ggg	cta	5047
329	Arg	Ala	Thr	Arg	Val	Ser	His	Gly	Arg	Val	Pro	Phe	Leu	Ala	Gly	Leu	
330				855				860						865			
332	cct	gac	agt	caa	gag	gag	aca	ctg	aac	ttc	ttg	atg	aac	agt	ggg	ttc	5095
333	Pro	Asp	Ser	Gln	Glu	Glu	Thr	Leu	Asn	Phe	Leu	Met	Asn	Ser	Gly	Phe	
334			870					875					880				
336	gat	ccc	aag	aag	caa	aag	tac	ttg	caa	gac	atc	gcc	tgg	gat	ctt	caa	5143
337	Asp	Pro	Lys	Lys	Gln	Lys	Tyr	Leu	Gln	Asp	Ile	Ala	Trp	Asp	Leu	Gln	
338		885					890					895					
340	aag	cgg	aaa	tgt	gac	acg	ttg	aag	tcc	aag	ctg	aac	atc	cgt	gtc	ggt	5191
341	Lys	Arg	Lys	Cys	Asp	Thr	Leu	Lys	Ser	Lys	Leu	Asn	Ile	Arg	Val	Gly	
342	900				905						910				915		
344	cga	tca	gca	tac	att	tac	atg	att	gcc	gat	ttc	tgg	ggt	gtg	ctt	gag	5239
345	Arg	Ser	Ala	Tyr	Ile	Tyr	Met	Ile	Ala	Asp	Phe	Trp	Gly	Val	Leu	Glu	
346				920					925					930			
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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date